



The New BLAST® Results Page

Enhanced graphical presentation and added functionality

<https://blast.ncbi.nlm.nih.gov/>

National Center for Biotechnology Information • National Library of Medicine • National Institutes of Health • Department of Health and Human Services

Scope

NCBI recently released an enhanced BLAST result display early 2019 (<https://go.usa.gov/xyq5Y>). This display will become the new default at the end of August, 2019, to coincide with the start of the new school year. The current default will be available as an alternative format until its retirement at the end of 2019. This new display:

- reduces the need of scrolling by placing each section of the BLAST results into their own tab
- makes result filtering easier by bringing the control to the front
- allows convenient download by arranging the option close to the result
- integrates the taxonomy report by placing its access as an new tab

Access to BLAST and the New BLAST Result Page

Access to NCBI BLAST web services through its homepage (blast.ncbi.nlm.nih.gov) remains the same as before. The change is in the layout of the display of the results after a search is completed. Before this display becomes default, there are two ways to access the new display: set it as default by clicking the checkbox in the advertisement, such as the one in the nucleotide search form (A), or using the link (B) at the top of the result page.

BLAST® >> **blastp suite** >> **RID-FV7PMBFR014** [Home](#) [Recent Results](#) [Saved Strategies](#) [Help](#)

BLAST Results

ⓘ Your search is limited to records that exclude: models (XM/XP)
[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Job title: **ref|np_001814|** [YouTube](#) [How to read this page](#) [Blast report description](#) **NEW** [Click here to see the new BLAST results page](#)

RID FV7PMBFR014 (Expires on 06-11 08:05 am)	Database Name nr
Query ID NP_001814.2	Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Description creatine kinase B-type Isoform 1 [Homo sapiens]	Program BLASTP 2.9.0+ Citation
Molecule type amino acid	
Query Length 381	

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#)
Analyze your query with [SmartBLAST](#)

[+ Graphic Summary](#)
[+ Descriptions](#)
[+ Alignments](#)

The general structure of the BLAST result page essentially stays the same, which contains the Summary, Graphical Overview, Descriptions table, and Alignments sections. The enhancements are in the following areas: 1) the Summary section is restructured to make the information more readable, 2) key post-search result filters are brought to the front, making them readily accessible, 3) remaining sections are reported in their own tabs below the Summary, 4) the Taxonomy report is integrated into this tab-formatted display, and 5) filters applied acts uniformly on Descriptions, Alignments, Taxonomy, as well as their download.

The Summary Section

The Summary section (shown below) is at the top of a result page. This section display is always on and is independent of which of the remaining sections is selected for display in the tabs below so you can know what you searched with and the database you searched against.

A. Navigational links at the top

- [Breadcrumbs](#) shows the hierarchy of the result page.
- [Links to key BLAST pages](#), such as “Recent Results” for a list of recently submitted BLAST searches, and “Saved Strategies” for saved search settings are to the right.

B. Functional links for this search

- [Edit Search](#) goes back to the search page to allow rerun of the search with adjusted settings.
- [Save Search](#) saves the search setting used for later use.
- [Search Summary](#) displays a table with summary statistics and search settings.

C. MyNCBI lets you save search settings permanently, log in here

Log in

A BLAST® » blastp suite » results for RID-FV7PMBFR014

B [Edit Search](#) [Save Search](#) [Search Summary](#) [How to read this report?](#) [BLAST Help Videos](#) [Back to Traditional Results Page](#) [BETA](#)

E Your search is limited to records that exclude: models (XM/XP)

D Job Title [ref|np_001814|](#)
 RID [FV7PMBFR014](#) Search expires on 06-11 08:05 am [Download All](#)
 Program BLASTP [Citation](#)
 Database nr [See details](#)
 Query ID [NP_001814.2](#)
 Description creatine kinase B-type isoform 1 [Homo sapiens]
 Molecule type amino acid
 Query Length 381
 Other reports [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#)

E Filter Results

Organism *only top 20 will appear* ☐ exclude
 Type common name, binomial, taxid or group name
[+ Add organism](#)

Percent Identity to E value to
[Filter](#) [Reset](#)

D. Summary provides information on different aspects of the search

- [Highlighted message box](#) displays reminder, warning, or errors if relevant.
- [Job Title](#) shows the first query's sequence id by default, for more better search identification customize it before submission.
- [RID](#) shows the assigned unique identifier to this search for sharing and problem reporting; [Download All](#) shows a list of options to save the complete search result in desired format (1), such as new XML (XML2), JSON, and CSV.
- [Results for](#) (not present for single query search) allows selection of the input query for which to show the search results.
- [Program](#) lists the search conducted, blastp in this case; [Citation](#) provides the reference to cite in your publication.
- [Database](#) names the target database searched; [See details](#) provides a text description of the content.
- [Query ID](#) is the query's sequence id for which the result is shown. If accession is used, it is linked to the record in NCBI database.
- [Description](#) is the title of the query sequence from its FASTA define.
- [Molecule type](#) shows the type of the sequence.
- [Query length](#) is the length of the current query.
- [Other reports](#) lists links to other report formats not integrated to the new tab-based display. Multiple alignment links to COBALT search, which is not available for nucleotide BLAST.

E. Filter Results

- [Organism](#) allows input of organism name (select from auto-suggested list) to filter the returned hits. Check the [exclude checkbox](#) to exclude selected organism from display. Need more organisms? click [Add organism](#) to add additional field.
- [Percent Identity](#) allows filtering of hits by degree of identity, such as between 94.74 and 94.76 percent.
- E Value filters result by hits' significance in Expect value, such as between 0.0001 and 5e-120 (5×10^{-120}).

Enter the desired values, then click [Filter](#) to update the result display. The Filter works through post-processing and does not change the returned search. Click [Reset](#) to see the initial set of results.

Text
 XML
 ASN.1
 JSON Seq-align
 Hit Table(text)
 Hit Table(csv)
 Multiple-file XML2
 Single-file XML2
 Multiple-file JSON
 Single-file JSON
SAM

1

The Descriptions tab (shown below) contains a summary table of hits found by BLAST. It is the default tab shown.

- Download provides a set of options to download the selected hits (as compared to Download All in the Summary section)
- Manage Columns lists all available columns of the table so you can check or uncheck for a customized table display.
- Show allows you to select how many hits are shown in the table.

- Select All toggle on and off checkboxes for all the hits. For custom selection, click on individual checkboxes to toggle selection of specific entries.
- GenPept retrieves the full protein records for selected entries in the Protein database.
- Graphics links to a graphical sequence viewer-based presentation of matches anchored by the query (1).
- Distance tree of results present the matches in a distance tree format (2)
- For phylogenetic analysis, use the Multiple alignment link instead (protein only).

C. Table header and rows

- Default sorting is by E value column (in bold). Click on another header to sort by that column (not applicable to Description and Accession columns).
- Titles in the Description column link to the cognate alignment in the Alignments section. Click a title to jump to that location in the Alignments section to examine the actual alignment.
- Entries in the Accession column link to the sequence record in the Protein database or Nucleotide (for blastn or tblastn searches).

[illegible]

